FIG. 1A

```
                1                                                   50
NOGO-R2         ~~~~~~MLPG LRRLLQAPAS AC...LLLML LA..LPLAAP SCPMLCTCYS
NOGO-R3         MSWQSGTTVT QSPVQAAQVS GCCVELLLLL LAGELPLGG. GCPRDCVCYP
NOGO-R1         ~~~~~~~~~~ ~~~~~MKRAS AGGSRLLAWV LWLQAWQVAA PCPGACVCYN
Consensus       ~~~~~~~~~~ ---------S -----LL--- L--------- -CP--C-CY-

                51                                                  100
NOGO-R2         SP.PTVSCQA NNFSSVPLSL PPSTQRLFLQ NNLIRTLRPG TFGS..NLLT
NOGO-R3         AP.MTVSCQA HNFAAIPEGI PEDSERIFLQ NNRITFLQQG HFSP..AMVT
NOGO-R1         EPKVTTSCPQ QGLQAVPVGI PAASQRIFLH GNRISHVPAA SFRACRNLTI
Consensus       -P--T-SC-- ------P--- P----R-FL- -N-I------ -F--------

                101                                                 150
NOGO-R2         LWLFSNNLST IYPGTFRHLQ ALEELDLGDN RHLRSLEPDT FQGLERLQSL
NOGO-R3         LWIYSNNITF IAPNTFEGFV HLEELDLGDN RQLRTLAPET FQGLVKLHAL
NOGO-R1         LWLHSNVLAR IDAAAFTGLA LLEQLDLSDN AQLRSVDPAT FHGLGRLHTL
Consensus       LW--SN---- I----F---- -LE-LDL-DN --LR---P-T F-GL--L--L

                151                                                 200
NOGO-R2         HLYRCQLSSL PGNIFRGLVS LQYLYLQENS LLHLQDDLFA DLANLSHLFL
NOGO-R3         YLYKCGLSAL PAGIFGGLHS LQYLYLQDNH IEYLQDDIFV DLVNLSHLFL
NOGO-R1         HLDRCGLQEL GPGLFRGLAA LQYLYLQDNA LQALPDDTFR DLGNLTHLFL
Consensus       -L--C-L--L ----F-GL-- LQYLYLQ-N- ---L-DD-F- DL-NL-HLFL

                201                                                 250
NOGO-R2         HGNRLRLLTE HVFRGLGSLD RLLLHGNRLQ GVHRAAFRGL SRLTILYLFN
NOGO-R3         HGNKLWSLGQ GIFRGLVNLD RLLLHENQLQ WVHHKAFHDL HRLTTLFLFN
NOGO-R1         HGNRISSVPE RAFRGLHSLD RLLLHQNRVA HVHPHAFRDL GRLMTLYLFA
Consensus       HGN------- --FRGL--LD RLLLH-N--- -VH--AF--L -RL--L-LF-
```

FIG. 1B

```
                251                                                 300
NOGO-R2         NSLASLPGEA LADLPSLEFL RLNANPWACD CRARPLWAWF QRARVSSSDV
NOGO-R3         NSLTELQGDC LAPLVALEFL RLNGNAWDCG CRARSLWEWL RRFRGSSSAV
NOGO-R1         NNLSALPTEA LAPLRALQYL RLNDNPWVCD CRARPLWAWL QKFRGSSSEV
Consensus       N-L--L---- LA-L--L--L RLN-N-W-C- CRAR-LW-W- ---R-SSS-V

                301                                                 350
NOGO-R2         TCATPPERQG RDLRALREAD FQAC...P.P AAPTRPGSRA ..........
NOGO-R3         PCATPELRQG QDLKLLRVED FRNC...TGP VSPHQIKSHT ..........
NOGO-R1         PCSLPQRLAG RDLKRLAAND LQGCAVATGP YHPIWTGRAT DEEPLGLPKC
Consensus       -C--P----G -DL--L---D ---C-----P --P------- ----------

                351                                                 400
NOGO-R2         .......RGN ..SSSNH.LY G.VAE..... AGAPPADPS. ..TLYRDLPA
NOGO-R3         ..LTTSDRAA ..RKEHHPSH G.ASRDKGHP HGHPPGSRSG YKKAGKNCTS
NOGO-R1         CQPDAADKAS VLEPGRPASA GNALKGRVPP GDSPPGNGSG PRHI.NDSPF
Consensus       ---------- ---------- G--------- ---PP---S- ----------

                401                                                 450
NOGO-R2         EDSRGR.... QGGDAPTE.D DYWGGY.... ......GGED QRGEQMCPGA
NOGO-R3         HRNRNQISKV SSGKELTELQ DYAPDYQHKF SFDIMPTARP KRKGKCARRT
NOGO-R1         GTLPGSAEPP LTAVRPEGSE P..PGFPTSG PRRRPGCSRK NRTRSHCRLG
Consensus       ---------- ---------- ---------- ---------- -R--------

                451                                             491
NOGO-R2         ACQAPPDSRG PALSAGLPSP LLCLLLLVPH HL~~~~~~~~ ~
NOGO-R3         PIRAPSGVQQ ASSGTALGAP LLAWILGLAV TLR~~~~~~~ ~
NOGO-R1         QAGSGGGGTG DSEGSGALPS LTCSLTPLGL ALVLWTVLGP C
Consensus       ---------- ---------- L--------- -L~~~~~~~~ ~
```

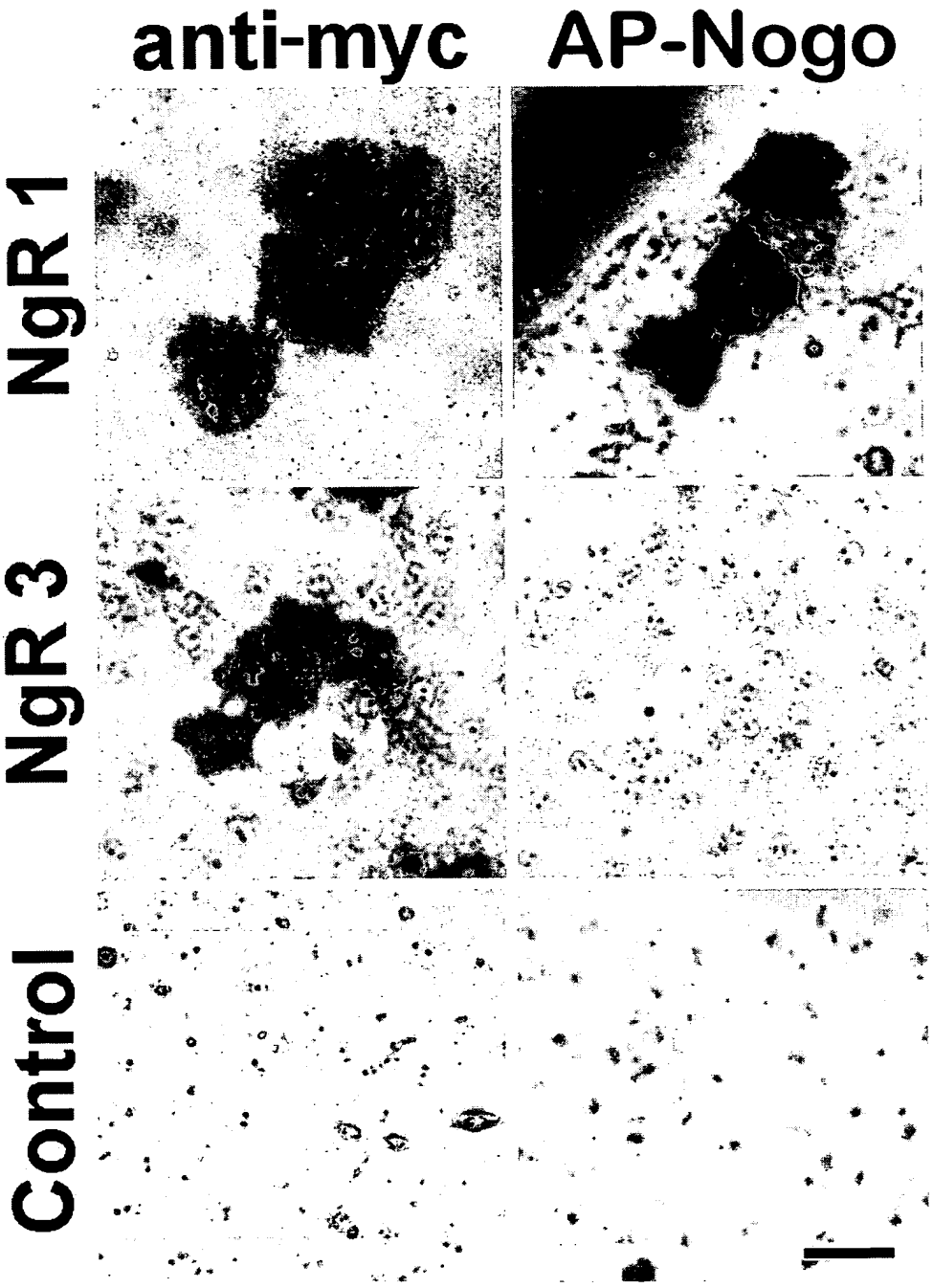

FIG. 2

1 50
Human NOGO-R1 ~~~~~~~~~~ ~~~~MKRASA GGSRLLAWVL WLQAWQVAAP CPGACVCYNE
Murine NOGO-R1 ~~~~~~~~~~ ~~~~MKRASS GGSRLLAWVL WLQAWRVATP CPGACVCYNE
Murine NOGO-R3 MSWQSGTTVT QSPVQAAQVS GCCVELLLLL LAGELPLGGG CPRDCVCYPA
Human NOGO-R3 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
Human NOGO-R2 ~~~~~~~~~~ MLPGLRRLLQ APASACLLLM LLALPLAAPS CPMLCTCYSS
Consensus ~~~~~~~~~~ ~~~~~~~~~~ ---------- ---------- CP--C-CY--
LRR NT
LRR 1
51 100
Human NOGO-R1 PKVTTSCPQQ GLQAVPVGIP AASQRIFLHG NRISHVPAAS FRACRNLTIL
Murine NOGO-R1 PKVTTSCPQQ GLQAVPTGIP ASSQRIFLHG NRISHVPAAS FQSCRNLTIL
Murine NOGO-R3 P.MTVSCQAH NFAAIPEGIP EDSERIFLQN NRITFLQQGH FSP..AMVTL
Human NOGO-R3 ~~~~~~~~~~ ~~~~~~EGIP VDSERVFLQN NRIGLLQPGH FSP..AMVTL
Human NOGO-R2 P.PTVSCQAN NFSSVPLSLP PSTQRLFLQN NLIRTLRPGT FGS..NLLTL
Consensus P--T-SC--- -----P---P ----R-FL-- N-I------- F---------L
LRR 2
LRR 3
101 150
Human NOGO-R1 WLHSNVLARI DAAAFTGLAL LEQLDLSDNA QLRSVDPATF HGLGRLHTLH
Murine NOGO-R1 WLHSNALARI DAAAFTGLTL LEQLDLSDNA QLHVVDPTTF HGLGHLHTLH
Murine NOGO-R3 WIYSNNITFI APNTFEGFVH LEELDLGDNR QLRTLAPETF QGLVKLHALY
Human NOGO-R3 WIYSNNITYI HPSTFEGFVH LEELDLGDNR QLRTLAPETF QGLVKLHALY
Human NOGO-R2 WLFSNNLSTI YPGTFRHLQA LEELDLGDNR HLRSLEPDTF QGLERLQSLH
Consensus W--SN----I ----F----- LE-LDL-DN- -L----P-TF -GL--L--L-
LRR 4
LRR 5
151 200
Human NOGO-R1 LDRCGLQELG PGLFRGLAAL QYLYLQDNAL QALPDDTFRD LGNLTHLFLH
Murine NOGO-R1 LDRCGLRELG PGLFRGLAAL QYLYLQDNNL QALPDNTFRD LGNLTHLFLH
Murine NOGO-R3 LYKCGLSALP AGIFGGLHSL QYLYLQDNHI EYLQDDIFVD LVNLSHLFLH
Human NOGO-R3 LYKCGLSALP AGVFGGLHSL QYLYLQDNHI EYLQDDIFVD LVNLSHLFLH
Human NOGO-R2 LYRCQLSSLP GNIFRGLVSL QYLYLQENSL LHLQDDLFAD LANLSHLFLH
Consensus L--C-L--L- ---F-GL--L QYLYLQ-N-- --L-D--F-D L-NL-HLFLH

FIG. 3

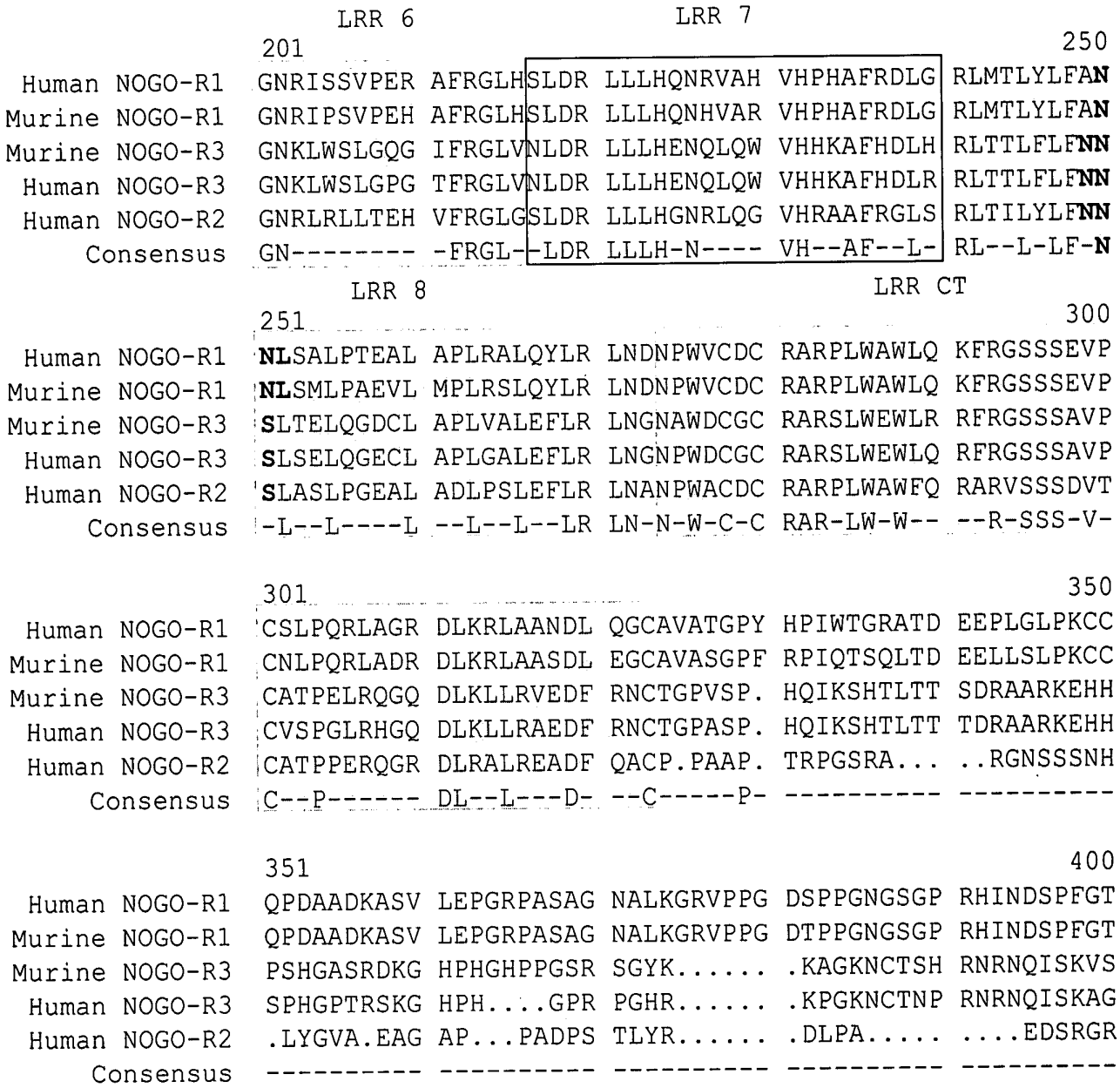
LRR 6
LRR 7
201
250
Human NOGO-R1 GNRISSVPER AFRGLHSLDR LLLHQNRVAH VHPHAFRDLG RLMTLYLFAN
Murine NOGO-R1 GNRIPSVPEH AFRGLHSLDR LLLHQNHVAR VHPHAFRDLG RLMTLYLFAN
Murine NOGO-R3 GNKLWSLGQG IFRGLVNLDR LLLHENQLQW VHHKAFHDLH RLTTLFLFNN
Human NOGO-R3 GNKLWSLGPG TFRGLVNLDR LLLHENQLQW VHHKAFHDLR RLTTLFLFNN
Human NOGO-R2 GNRLRLLTEH VFRGLGSLDR LLLHGNRLQG VHRAAFRGLS RLTILYLFNN
Consensus GN-------- -FRGL--LDR LLLH-N---- VH--AF--L- RL--L-LF-N
LRR 8
LRR CT
251
300
Human NOGO-R1 NLSALPTEAL APLRALQYLR LNDNPWVCDC RARPLWAWLQ KFRGSSSEVP
Murine NOGO-R1 NLSMLPAEVL MPLRSLQYLR LNDNPWVCDC RARPLWAWLQ KFRGSSSEVP
Murine NOGO-R3 SLTELQGDCL APLVALEFLR LNGNAWDCGC RARSLWEWLR RFRGSSSAVP
Human NOGO-R3 SLSELQGECL APLGALEFLR LNGNPWDCGC RARSLWEWLQ RFRGSSSAVP
Human NOGO-R2 SLASLPGEAL ADLPSLEFLR LNANPWACDC RARPLWAWFQ RARVSSSDVT
Consensus -L--L----L --L--L--LR LN-N-W-C-C RAR-LW-W-- --R-SSS-V-
301
350
Human NOGO-R1 CSLPQRLAGR DLKRLAANDL QGCAVATGPY HPIWTGRATD EEPLGLPKCC
Murine NOGO-R1 CNLPQRLADR DLKRLAASDL EGCAVASGPF RPIQTSQLTD EELLSLPKCC
Murine NOGO-R3 CATPELRQGQ DLKLLRVEDF RNCTGPVSP. HQIKSHTLTT SDRAARKEHH
Human NOGO-R3 CVSPGLRHGQ DLKLLRAEDF RNCTGPASP. HQIKSHTLTT TDRAARKEHH
Human NOGO-R2 CATPPERQGR DLRALREADF QACP.PAAP. TRPGSRA... ..RGNSSSNH
Consensus C--P------ DL--L---D- --C-----P- ---------- ----------
351
400
Human NOGO-R1 QPDAADKASV LEPGRPASAG NALKGRVPPG DSPPGNGSGP RHINDSPFGT
Murine NOGO-R1 QPDAADKASV LEPGRPASAG NALKGRVPPG DTPPGNGSGP RHINDSPFGT
Murine NOGO-R3 PSHGASRDKG HPHGHPPGSR SGYK..... .KAGKNCTSH RNRNQISKVS
Human NOGO-R3 SPHGPTRSKG HPH....GPR PGHR..... .KPGKNCTNP RNRNQISKAG
Human NOGO-R2 .LYGVA.EAG AP...PADPS TLYR..... .DLPA..... ....EDSRGR
Consensus ---------- ---------- ---------- ---------- ----------

FIG. 3, cont.

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                401                                                 450
Human NOGO-R1   LPGSAEPPLT AVRPEGSEPP GF...PTSGP RRRPGCSRKN RTRSHCRLGQ
Murine NOGO-R1  LPSSAEPPLT ALRPGGSEPP GL...PTTGP RRRPGCSRKN RTRSHCRLGQ
Murine NOGO-R3  .SGKELTELQ DYAPDYQHKF SFDIMPTARP KRKGKCARRT PIRAPSGVQQ
Human NOGO-R3   .AGKQAPELP DYAPDYQHKF SFDIMPTARP KRKGKCARRT PIRAPSGVQQ
Human NOGO-R2   .QGGDAPTED DYWGGY.... ......GGED QRGEQMCPGA ACQAPPD...
    Consensus   ---------- ---------- ---------- -R-------- ----------

                451                 Putative GPI Signals  490
Human NOGO-R1   AGSGGGGTGD SEGSGALPSL TCSLTPLGLA LVLWTVLGPC
Murine NOGO-R1  AGSGASGTGD AEGSGALPAL ACSLAPLGLA LVLWTVLGPC
Murine NOGO-R3  .......... ..ASSGTALG APLLAWILGL AVTLR~~~~~
Human NOGO-R3   .......... ..ASSASSLG ASLLAWTLGL AVTLR~~~~~
Human NOGO-R2   .......... ..SRGPALSA GLPS PLLCL LLLVPHHL~~
    Consensus   ---------- --------- ---------- ----------
```

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FIG. 3, cont.